

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 13:53:26 ; Search time 22 Seconds
(Without alignments)
41.476 Million cell updates/sec

Title: US-09-914-213-2

Perfect score: 116
Sequence: 1 GLEISEINEEDLKECFDDME 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	116	100.0	1480 1 CFTR_HUMAN	P13569 homo sapien
2	106	91.4	1481 1 CFTR_BOVIN	P35071 bos taurus
3	106	91.4	1481 1 CFTR_SHEEP	Q00555 ovis aries
4	103	88.8	1450 1 CFTR_RABBIT	Q00554 oryctolagus
5	97	83.6	524 1 CFTR_RAT	P34158 rattus norv
6	94	81.0	1485 1 CFTR_XENTIA	P26363 xenopus lae
7	87	75.0	1476 1 CFTR_MOUSE	P26361 mus musculu
8	87	75.0	1492 1 CFTR_SQUAC	P26362 squatus aca
9	57	49.1	378 1 LUXE_VIBHA	P14286 vibrio harv
10	54	46.6	626 1 RNT1_MOUSE	Q99mw7 mus musculu
11	50	43.1	631 1 ETED_YEAST	Q08822 s probale
12	49	42.2	257 1 ETXA_STRAU	P13163 staphylococ
13	49	42.2	257 1 ETXA_STRAU	P12993 staphylococ
14	49	42.2	457 1 HEMM_HELPU	Q25376 helicobacte
15	48.5	41.8	565 1 YHXA_BACSU	P18159 bacillus su
16	48	41.4	457 1 HEMM_HELPU	Q921h0 helicobacte
17	47	40.5	603 1 LEPA_SYNY3	P74751 synchocyste
18	47	40.5	121 1 AB11_HUMAN	O95342 homo sapien
19	46	39.7	599 1 PRIM_BACHD	O9k444 bacillus ha
20	46	39.7	706 1 NUCL_MOUSE	P09405 mus musculu
21	46	39.7	1328 1 FINC_PLEMA	O91289 pleurodeles
22	46	39.7	1882 1 POL2_TRSVR	P25247 tomato ring
23	45	38.8	201 1 RACG_DICDI	O99s80 dictyostell
24	45	38.8	260 1 RS2_BORBU	O51149 borrelia bu
25	45	38.8	442 1 VAN1_CANAL	O00314 candida alb
26	45	38.8	593 1 NTDA_ENTHR	O08635 enterococcu
27	45	38.8	887 1 MCM2_DROME	P49335 drosophila
28	44.5	38.4	386 1 NESG_HUMAN	O9u116 homo sapien
29	44	37.9	240 1 Y124_THEMA	O9wx88 thermocoga
30	44	37.9	373 1 LUXE_PHELE	P29334 photobacter
31	44	37.9	3951 1 VGFL_IBVB	P27920 avian infec
32	43.5	37.5	273 1 SC65_YEAST	P29478 saccharomyc
33	43.5	37.5	614 1 IF2_UREPA	O9p9h1 ureaplasma

34	43	37.1	173 1 LEPA_MYCH	O9z2h8 mycoplasma
35	43	37.1	210 1 VP28_CABEL	O9n226 caenorhabd1
36	43	37.1	264 1 KKA3_ENTFA	P00554 enterococcu
37	43	37.1	358 1 ALF_YEAST	P14540 saccharomyc
38	43	37.1	437 1 DNAA_MYCGE	P35888 mycoplasma
39	43	37.1	459 1 TRME_BACSU	P25811 bacillus su
40	43	37.1	554 1 Y478_RICPR	O9z466 rickettsia
41	43	37.1	713 1 NUCL_MESAU	P08199 mesocricetu
42	43	37.1	756 1 MLH1_HUMAN	P40692 homo sapien
43	43	37.1	760 1 MLH1_MOUSE	O91K91 mus musculu
44	43	37.1	1101 1 P11G_HUMAN	P48736 homo sapien
45	42.5	36.6	842 1 PHSN_VICFA	P53537 vicla feba

ALIGNMENTS

RESULT 1	CFTR_HUMAN	STANDARD:	PRT: 1480 AA.
AC	P13569:		
DT	01-JAN-1990 (Rel. 13, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Cystic fibrosis transmembrane conductance regulator (CFTR) (Camp-		
DE	dependent chloride channel).		
GN	CFTR OR ABCC7.		
OS	Homo sapiens (human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_Taxid:9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-69368940; PubMed-2475911;		
RA	Riordan J.R., Rommens J.M., Kerem B., Alon N., Rozmahel R.,		
RA	Grzelczak Z., Zielenski J., Lok S., Plavsky N., Chou J.-L.,		
RA	Drumm M.L., Iannuzzi M.C., Collins F.S., Tsui L.-C.;		
RT	"Identification of the cystic fibrosis gene: cloning and		
RT	characterization of complementary DNA.";		
RL	Science 245:1066-1073(1989).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-91257831; PubMed-1710598;		
RA	Zielenski J., Rozmahel R., Bozon D., Kerem B., Grzelczak Z.,		
RA	Riordan J.R., Rommens J., Tsui L.-C.;		
RT	"Genomic DNA sequence of the cystic fibrosis transmembrane		
RT	conductance regulator (CFTR) gene.";		
RL	Genomics 10:214-228(1991).		
RN	[3]		
RP	3D-STRUCTURE MODELING OF 425-638.		
RX	MEDLINE-98176720; PubMed-9517543;		
RA	Hoedemaecker F.J., Davidson A.R., Rose D.R.;		
RT	"A model for the nucleotide-binding domains of ABC transporters based		
RT	on the large domain of aspartate aminotransferase.";		
RL	Proteins 30:275-286(1998).		
RN	[4]		
RP	PHOSPHORYLATION SITES.		
RX	MEDLINE-92316961; PubMed-1377674;		
RA	Picciotto M.R., Conn J.A., Bertuzzi G., Greengard P., Nairn A.C.;		
RT	"Phosphorylation of the cystic fibrosis transmembrane conductance		
RT	regulator.";		
RL	J. Biol. Chem. 267:12742-12752(1992).		
RN	[5]		
RP	PHOSPHORYLATION SITES.		
RX	MEDLINE-98046756; PubMed-9385646;		
RA	Neville D.C.A., Rozanas C.R., Rice E.M., Gruls D.B., Verhman A.S.,		
RT	Townsend R.R.;		
RT	"Evidence for phosphorylation of serine 753 in CFTR using a novel		
RT	metal-ion affinity resin and matrix-assisted laser desorption mass		
RL	spectrometry.";		
RL	Protein Sci. 6:2436-2445(1997).		
RN	[6]		
RP	REVIEW.		

RX MEDLINE=92339790; PubMed=1378801;
 RA McIntosh I., Cutting G.R.;
 RT "Cystic fibrosis transmembrane conductance regulator and the etiology
 of pathogenesis of cystic fibrosis.";
 RL FASEB J. 6:2775-2782(1992).
 RN [7]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=93250808; PubMed=1284534;
 RA Tsui L.-C.;
 RT "Mutations and sequence variations detected in the cystic fibrosis
 transmembrane conductance regulator (CFTR) gene: a report from the
 Cystic Fibrosis Genetic Analysis Consortium.";
 RL Hum. Mutat. 1:197-203(1992).
 RN [8]
 RP VARIANTS CF.
 RX MEDLINE=90326187; PubMed=1695717;
 RA Cutting G.R., Kasch L.M., Rosenstein B.J., Zielenski J., Tsui L.-C.,
 RA Antonarakis S.E., Kazazian H.H. Jr.;
 RT "A cluster of cystic fibrosis mutations in the first
 nucleotide-binding fold of the cystic fibrosis conductance regulator
 protein.";
 RL Nature 346:366-369(1990).
 RN [9]
 RP VARIANTS CF.
 RX MEDLINE=91046014; PubMed=2236053;
 RA Kelem B.-S., Zielenski J., Markiewicz D., Bozon D., Gazit E.,
 RA Yahav J., Kennedy D., Riordan J.R., Collins F.S., Rommens J.M.,
 RA Tsui L.-C.;
 RT "Identification of mutations in regions corresponding to the two
 putative nucleotide (ATP)-binding folds of the cystic fibrosis
 gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8447-8451(1990).
 RN [10]
 RP VARIANTS CF.
 RX MEDLINE=91257839; PubMed=1710600;
 RA White M.B., Krueger L.J., Holcslaw D.S. Jr., Gerrard B.C.,
 RA Stewart C., Qutlell L., Dolganov G., Baranov V., Ivashchenko T.,
 RA Kaponov N.I., Sebastiao G., Castiglione O., Dean M.;
 RT "Detection of three rare frameshift mutations in the cystic fibrosis
 gene in an African-American (CF444delA), an Italian (CF2522insC), and
 a Soviet (CF3821delT).";
 RL Genomics 10:266-269(1991).
 RN [11]
 RP VARIANTS CF PHE-520 AND HIS-1291.
 RX MEDLINE=93244747; PubMed=1284466;
 RA Jones C.T., McIntosh I., Keston M., Ferguson A., Brock D.J.H.;
 RT "Three novel mutations in the cystic fibrosis gene detected by
 chemical cleavage: analysis of variant splicing and a nonsense
 mutation.";
 RL Hum. Mol. Genet. 1:11-17(1992).
 RN [12]
 RP VARIANTS CF MET-1283.
 RX MEDLINE=93244771; PubMed=1284468;
 RA Cheddie J.P., Meredith A.L., Al-Jader L.N.;
 RT "A new missense mutation (R1283M) in exon 20 of the cystic fibrosis
 transmembrane conductance regulator gene.";
 RL Hum. Mol. Genet. 1:123-125(1992).
 RN [13]
 RP VARIANTS CF PRO-1255.
 RX MEDLINE=93250788; PubMed=1284530;
 RA Lissens W., Bonduelle M., Malfroot A., Dab I., Liebaers I.;
 RT "A serine to proline substitution (S1255P) in the second nucleotide
 binding fold of the cystic fibrosis gene.";
 RL Hum. Mol. Genet. 1:441-442(1992).
 RN [14]
 RP VARIANTS CF LYS-92 AND CYS-117.
 RX MEDLINE=93250787; PubMed=1284529;
 RA Shackleton S., Beards F., Harris A.;
 RT "Detection of novel and rare mutations in exon 4 of the cystic
 fibrosis gene by SSCP.";
 RL Hum. Mol. Genet. 1:439-440(1992).
 RN [15]
 RP VARIANTS CF LYS-1101.

RX MEDLINE=93190992; PubMed=7680525;
 RA Zielenski J., Fujiwara T.M., Markiewicz D., Paradis A.J.,
 RA Anacleto A.I., Richards B., Schwartz R.H., Klinger K.W., Tsui L.C.,
 RA Morgan K.;
 RT "Identification of the M101K mutation in the cystic fibrosis
 transmembrane conductance regulator (CFTR) gene and complete
 detection of cystic fibrosis mutations in the Hutterite population.";
 RL Am. J. Hum. Genet. 52:609-615(1993).
 RN [16]
 RP VARIANTS CF V-1052; R-1061; L-1066; Q-1070; R-1085 AND R-1101.
 RX MEDLINE=93252404; PubMed=7683628;
 RA Mercier B., Lissens W., Novelli G., Kalaydjieva L., De Arce M.,
 RA Kapranov N., Kilian N.C., Lenoir G., Chauveau P., Lenaerts C.,
 RA Rault G., Cashman S., Sangiulio F., Andrezet M.P., Dallapiccola B.,
 RA Guillemit H., Bonduelle M., Liebaers I., Quere I., Verlingue C.,
 RA Ferec C.;
 RT "Identification of eight novel mutations in a collaborative analysis
 of a part of the second transmembrane domain of the CFTR gene.";
 RL Genomics 16:296-297(1993).
 RN [17]
 RP VARIANTS CF LYS-92.
 RX MEDLINE=93258355; PubMed=7683954;
 RA Nunes V., Chillon M., Doerk T., Tuemmler B., Casals T., Estivill X.;
 RT "A new missense mutation (E92K) in the first transmembrane domain of
 the CFTR gene causes a benign cystic fibrosis phenotype.";
 RL Hum. Mol. Genet. 2:79-80(1993).
 RN [18]
 RP VARIANTS CF SER-205.
 RX MEDLINE=94093573; PubMed=7505694;
 RA Chillon M., Casals T., Nunes V., Gimenez J., Ruiz E.P., Estivill X.;
 RT "Identification of a new missense mutation (P205S) in the first
 transmembrane domain of the CFTR gene associated with a mild cystic
 fibrosis phenotype.";
 RL Hum. Mol. Genet. 2:1741-1742(1993).
 RN [19]
 RP VARIANTS CF.
 RX MEDLINE=94080255; PubMed=7504699;
 RA Gasparini P., Marigo C., Bisceglia G., Nicolis E., Zelante L.,
 RA Bombieri C., Borgo G., Pignatti P.F., Cabrioli G.;
 RT "Screening of 62 mutations in a cohort of cystic fibrosis patients
 from north eastern Italy: their incidence and clinical features of
 defined genotypes.";
 RL Hum. Mutat. 2:389-394(1993).
 RN [20]
 RP VARIANTS CYS-31; ILE-1220; CF LEU-912; TYR-949; PRO-1065; PRO-1071.
 RX MEDLINE=94375072; PubMed=7522211;
 RA Ghaneb N., Costes B., Girodon E., Martin J., Fanen P., Goossens M.;
 RT "Identification of eight mutations and three sequence variations in
 the cystic fibrosis transmembrane conductance regulator (CFTR)
 gene.";
 RL Genomics 21:434-436(1994).
 RN [21]
 RP VARIANTS CF PRO-346.
 RX MEDLINE=9422417; PubMed=7513296;
 RA Botva K., Papageorgiou E., Georgiou C., Anastasiadis M.,
 RA Middleton L.T., Constantinou-Deltas C.D.;
 RT "Novel cystic fibrosis mutation associated with mild disease in
 Cypriot patients.";
 RL Hum. Genet. 93:529-532(1994).
 RN [22]
 RP VARIANTS CF TYR-199; SER-619; ARG-1005 AND ARG-1291.
 RX MEDLINE=95048290; PubMed=7525450;
 RA Doerk T., Mekus F., Schmidt K., Boshammer J., Fislage R., Heuer T.,
 RA Dziadek V., Neumann T., Kaelin N., Wulbrand U., Wolf B.,
 RA von der Hardt H., Maass G., Tuemmler B.;
 RT "Detection of more than 50 different CFTR mutations in a large group
 of German cystic fibrosis patients.";
 RL Hum. Genet. 94:533-542(1994).
 RN [23]
 RP VARIANTS CF GLU-1249.
 RX MEDLINE=94333927; PubMed=7520022;
 RA Grell I., Wagner K., Rosenkranz W.;
 RT "A new missense mutation G1249E in exon 20 of the cystic fibrosis

Query Match 100.0%; Score 116; DB 1; Length 1480;
 Best Local Similarity 100.0%; Pred. No. 7e-08;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GLEISEEINEDLKECFDDME 22
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 DB 817 GLEISEEINEDLKECFDDME 838

RESULT 2

CFTR_BOVIN STANDARD; PRT; 1481 AA.
 AC P35071;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cystic fibrosis transmembrane conductance regulator (CFTR) (CAMP-dependent chloride channel).
 GN CFTR OR ABCG7.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bovinae; Bos.
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92042228; PubMed=1719001;
 RT Diamond G., Scanlin T.F., Zaslloff M.A., Bevins C.L.;
 RT "A cross-species analysis of the cystic fibrosis transmembrane conductance regulator. Potential functional domains and regulatory sites.";
 RT J. Biol. Chem. 266:22761-22769(1991).
 RL -1- FUNCTION: INVOLVED IN THE TRANSPORT OF CHLORIDE IONS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.

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 CC -----
 DR EMBL: M76128; AAA30772.1; -
 DR PIR: A39323; A39323.
 DR HSSP: P13569; JMBD.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR001140; ABC_transport.
 DR InterPro: IPR005291; CAMP_cl_channel.
 DR Pfam: PF00005; ABC_tran; 2.
 DR Pfam: PF00664; ABC_membrane; 2.
 DR ProDom: PD000006; ABC_transport; 2.
 DR SMART: SM00382; AAA; 1.
 DR TIGRFAMs: TIGR00953; 3a01202; 1.
 DR TIGRFAMs: TIGR01271; CFTR_protein; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; Transmembrane; Transport; Glycoprotein; Repeat; Ionic channel; Phosphorylation.

FT TRANSMEM 118 138 1 (POTENTIAL).
 FT TRANSMEM 195 215 3 (POTENTIAL).
 FT TRANSMEM 221 241 4 (POTENTIAL).
 FT TRANSMEM 308 326 5 (POTENTIAL).
 FT TRANSMEM 331 350 6 (POTENTIAL).
 FT TRANSMEM 437 464 7 (POTENTIAL).
 FT TRANSMEM 860 880 8 (POTENTIAL).
 FT TRANSMEM 912 932 9 (POTENTIAL).
 FT TRANSMEM 991 1011 10 (POTENTIAL).
 FT TRANSMEM 1014 1034 11 (POTENTIAL).
 FT TRANSMEM 1103 1123 11 (POTENTIAL).

FT TRANSMEM 1129 1149 12 (POTENTIAL).
 FT NP_BIND 1245 1252 ATP (BY SIMILARITY).
 FT MOD_RES 659 659 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT MOD_RES 685 685 PHOSPHORYLATION (BY PKC) (POTENTIAL).
 FT MOD_RES 699 699 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT MOD_RES 736 736 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT MOD_RES 767 767 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT MOD_RES 790 790 PHOSPHORYLATION (BY PKC) (POTENTIAL).
 FT MOD_RES 795 795 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT MOD_RES 813 813 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 SO SEQUENCE 1481 AA; 167758 MW; 83A706855C496AD7 CRC64.

Query Match 91.4%; Score 106; DB 1; Length 1481;
 Best Local Similarity 86.4%; Pred. No. 1.5e-06;
 Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 GLEISEEINEDLKECFDDME 22
 ||||||||||||||||||||
 DB 817 GLEISEEINEDLKECFDDME 838

RESULT 3

CFTR_SHEEP STANDARD; PRT; 1481 AA.
 AC Q00555; Q28544;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cystic fibrosis transmembrane conductance regulator (CFTR) (CAMP-dependent chloride channel).
 GN CFTR OR ABCG7.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Caprinae; Ovis.
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=95199336; PubMed=7534416;
 RT Tebbutt S.J., Wardle C.J., Hill D.F., Harris A.;
 RT "Molecular analysis of the ovine cystic fibrosis transmembrane conductance regulator gene.";
 RT Proc. Natl. Acad. Sci. U.S.A. 92:2293-2297(1995).
 RL [2]

RP SEQUENCE OF 600-776 FROM N.A.
 RX MEDLINE=92042228; PubMed=1719001;
 RA Diamond G., Scanlin T.F., Zaslloff M.A., Bevins C.L.;
 RA "A cross-species analysis of the cystic fibrosis transmembrane conductance regulator. Potential functional domains and regulatory sites.";
 RT J. Biol. Chem. 266:22761-22769(1991).
 RN [3]

RP VARIANT GLN-297.
 RX MEDLINE=98357018; PubMed=9691989;
 RA Tebbutt S.J., Lakeman M.B., Wilson-Wheeler J.C., Hill D.F.;
 RA "Genetic variation within the ovine cystic fibrosis transmembrane conductance regulator gene.";
 RT Mutat. Res. 382:93-98(1998).

CC -1- FUNCTION: INVOLVED IN THE TRANSPORT OF CHLORIDE IONS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
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 CC -----

DR EMBL: U20418; AAA86600.1; -
 DR EMBL: M96682; AAA31514.1; -
 DR PIR: B39323; B39323.

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DR HSSP: P13569; 1NBD.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transportr.
DR InterPro: IPR001140; ABCtransportrTM.
DR InterPro: IPR005291; CAMP_cl_channel.
DR Pfam: PF00005; ABC_tran. 2.
DR Pfam: PF00664; ABC_membrane. 2.
DR ProDom: PD000006; ABC_transportr; 2.
DR SMART: SM00382; AAA; 1.
DR TIGRfams: TIGR00953; 3a01202; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
DR ATP-binding: Transmembrane; Transport; Glycoprotein; Repeat;
  Ionic channel; Phosphorylation; Polymorphism.
KW TRANSMEM 81
FT TRANSMEM 103
FT TRANSMEM 118
FT TRANSMEM 138
FT TRANSMEM 195
FT TRANSMEM 221
FT TRANSMEM 241
FT TRANSMEM 308
FT TRANSMEM 331
FT TRANSMEM 350
FT NP_BIND 457
FT TRANSMEM 464
FT TRANSMEM 860
FT TRANSMEM 912
FT TRANSMEM 991
FT TRANSMEM 1014
FT TRANSMEM 1034
FT TRANSMEM 1103
FT TRANSMEM 1129
FT TRANSMEM 1245
FT NP_BIND 1252
FT MOD_RES 659
FT MOD_RES 685
FT MOD_RES 699
FT MOD_RES 736
FT MOD_RES 767
FT MOD_RES 790
FT MOD_RES 795
FT MOD_RES 813
FT VARIANT 297
FT CONFLICT 600
FT CONFLICT 668
SQ SEQUENCE 1481 AA; 167926 MW; FCA6B9E82056E32 CRC64;

Query Match 91.4%; Score 106; DB 1; Length 1481;
Best local Similarity 86.4%; Pred. No. 1.5e-06;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEISEINEEDLKCEFPDME 22
DB 817 GLEISEINEEDLRCFDDVE 838

RESULT 4
CSTR_RABIT STANDARD; PRT; 1450 AA.
ID CSTR_RABIT
AC 000554;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator (CFTR) (CAMP-
  dependent chloride channel).
GN CFTR OR ABC7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart ventricle;
RX MEDLINE=96270540; PubMed=8692817;
RA Hart P.H., Warth J.D., Levesque P.C., Collier M.L., Geary Y.,
RA Horowitz B., Hume J.R.;
RT "Cystic fibrosis gene encodes a CAMP-dependent chloride channel in
  heart.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:6343-6348(1996).

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RN [2]
RP SEQUENCE OF 574-745 FROM N.A.
RX MEDLINE=92042228; PubMed=1719001;
RA Diamond G., Scanlin J.F., Zaslouff M.A., Beyins C.L.;
RT "A cross-species analysis of the cystic fibrosis transmembrane
  conductance regulator. Potential functional domains and regulatory
  sites.";
RL J. Biol. Chem. 266:22761-22769(1991).
CC - FUNCTION: INVOLVED IN THE TRANSPORT OF CHLORIDE IONS.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
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CC -----
DR EMBL: U40227; AAC48608.1; -.
DR EMBL: M96681; AAA31200.1; -.
DR FIR: E39323; E39323.
DR HSSP: P13569; 1NBD.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transportr.
DR InterPro: IPR001140; ABCtransportrTM.
DR InterPro: IPR005291; CAMP_cl_channel.
DR Pfam: PF00005; ABC_tran. 2.
DR Pfam: PF00664; ABC_membrane. 2.
DR ProDom: PD000006; ABC_transportr; 2.
DR SMART: SM00382; AAA; 1.
DR TIGRfams: TIGR00953; 3a01202; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
DR ATP-binding: Transmembrane; Transport; Glycoprotein; Repeat;
  Ionic channel; Phosphorylation.
KW TRANSMEM 81
FT TRANSMEM 103
FT TRANSMEM 118
FT TRANSMEM 138
FT TRANSMEM 165
FT TRANSMEM 191
FT TRANSMEM 211
FT TRANSMEM 278
FT TRANSMEM 301
FT TRANSMEM 320
FT NP_BIND 428
FT NP_BIND 435
FT TRANSMEM 830
FT TRANSMEM 850
FT TRANSMEM 882
FT TRANSMEM 961
FT TRANSMEM 981
FT TRANSMEM 984
FT TRANSMEM 1004
FT TRANSMEM 1073
FT TRANSMEM 1093
FT TRANSMEM 1099
FT TRANSMEM 1119
FT NP_BIND 1214
FT NP_BIND 1221
FT CONFLICT 647
FT CONFLICT 685
FT CONFLICT 701
FT CONFLICT 719
SQ SEQUENCE 1450 AA; 164629 MW; FAF583B5D205E CRC64;

Query Match 88.8%; Score 103; DB 1; Length 1450;
Best local Similarity 86.4%; Pred. No. 3.8e-06;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEISEINEEDLKCEFPDME 22
DB 787 GLEISEINEEDLKCEFPDMD 808

RESULT 5
CSTR_RAT STANDARD; PRT; 524 AA.
ID CSTR_RAT
AC P34158;
DT 01-FEB-1994 (Rel. 28, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

```

DE Cystic fibrosis transmembrane conductance regulator (CFTR) (CAMP-
 DE dependent chloride channel) (Fragments).
 GN CFTR OR ABC7.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteleia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE OF 1-17 FROM N.A.
 RX MEDLINE=95072572; PubMed=7526924;
 RA Denamur E., Chehab F.F.;
 RT "Analysis of the mouse and rat CFTR promoter regions.";
 RL Hum. Mol. Genet. 3:1089-1094(1994).
 RN [2]
 RP SEQUENCE OF 18-524 FROM N.A.
 RX MEDLINE=93122796; PubMed=1282491;
 RA Trezise A.E., Szpirer C., Buchwald M.;
 RT "Localization of the gene encoding the cystic fibrosis transmembrane
 RT conductance regulator (CFTR) in the rat to chromosome 4 and
 RT implications for the evolution of mammalian chromosomes.";
 RL Genomics 14:869-874(1992).
 CC -1- FUNCTION: INVOLVED IN THE TRANSPORT OF CHLORIDE IONS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: L26098; AAA73561.1; -;
 DR EMBL: M89906; AAA40918.1; -;
 DR HSSP: P13569; INBD.
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR001140; ABCtransprtTM.
 DR Pfam: PF00005; ABC_tran; 1.
 DR ProDom: PD000006; ABC_transport; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 KM ATP-binding; Transmembrane; Transport; Glycoprotein; Repeat;
 KW Ionic channel; Phosphorylation.
 FT NON_CONS 17 18
 FT TRANSMEM 391 411 7 (POTENTIAL).
 FT TRANSMEM 443 463 8 (POTENTIAL).
 FT NON_TER 524 524
 SQ SEQUENCE 524 AA: 59250 MW: 79444A96ED5924A CRC64;
 QY Query Match 83.6%; Score 97; DB 1; Length 524;
 Best Local Similarity 90.0%; Pred. No. 8.6e-06;
 Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 DB 2 LEISEINDEDKCECFDDM 21
 DB 349 LNTETINDEDKCECFDDM 368
 RESULT 6
 CFTR_XENLA
 ID CFTR_XENLA STANDARD; PRT; 1485 AA.
 AC P26363;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cystic fibrosis transmembrane conductance regulator (CFTR) (CAMP-
 DE dependent chloride channel).
 GN CFTR OR ABC7.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93244789; PubMed=1284470;
 RA Tucker S.J., Tannahill D., Higgins C.F.;
 RT "Identification and developmental expression of the Xenopus laevis
 RT cystic fibrosis transmembrane conductance regulator gene.";
 RL Hum. Mol. Genet. 1:77-82(1992)
 CC -1- FUNCTION: INVOLVED IN THE TRANSPORT OF CHLORIDE IONS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: X65256; CAA6348.1; -;
 DR PIR: S23756; S23756.
 DR HSSP: P13569; INBD.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR001140; ABCtransprtTM.
 DR InterPro: IPR005291; CAMP_cl_channel.
 DR Pfam: PF00005; ABC_tran; 2.
 DR ProDom: PD000006; ABC_transport; 2.
 DR SMART: SM00382; AAA; 2.
 DR TIGRFA: TIGR00953; 3a01202; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 DR ATP-binding; Transmembrane; Transport; Glycoprotein; Repeat;
 KW Ionic channel; Phosphorylation.
 KM TRANSMEM 82 104 1 (POTENTIAL).
 FT TRANSMEM 119 139 2 (POTENTIAL).
 FT TRANSMEM 196 216 3 (POTENTIAL).
 FT TRANSMEM 222 242 4 (POTENTIAL).
 FT TRANSMEM 309 329 5 (POTENTIAL).
 FT TRANSMEM 332 351 6 (POTENTIAL).
 FT NP_BIND 459 466 7 (POTENTIAL).
 FT TRANSMEM 862 882 8 (POTENTIAL).
 FT TRANSMEM 917 937 9 (POTENTIAL).
 FT TRANSMEM 996 1016 10 (POTENTIAL).
 FT TRANSMEM 1039 1039 11 (POTENTIAL).
 FT TRANSMEM 1108 1128 11 (POTENTIAL).
 FT TRANSMEM 1134 1155 11 (POTENTIAL).
 FT NP_BIND 1247 1254 ATP (BY SIMILARITY).
 FT CARBOHYD 894 894 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 900 900 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 1485 AA: 168895 MW: 285959B7DB3389 CRC64;
 QY Query Match 81.0%; Score 94; DB 1; Length 1485;
 Best Local Similarity 81.0%; Pred. No. 6.2e-05;
 Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 DB 2 LEISEINDEDKCECFDDME 22
 DB 820 LEVSEINDEDKCECFDDTD 840
 RESULT 7
 CFTR_MOUSE
 ID CFTR_MOUSE STANDARD; PRT; 1476 AA.
 AC P26361; O63893; O63894; O93K06;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cystic fibrosis transmembrane conductance regulator (CFTR) (CAMP-
 DE dependent chloride channel).
 GN CFTR OR ABC7.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91301683; PubMed=1712752;
 RA Tata F., Stalter P., Wicking C., Halford S., Kruyer H., Lench N.J.,
 RA Scambler P.J., Hansen C., Birman J.C., Williamson R., Wainwright B.J.;
 RT "Cloning the mouse homolog of the human cystic fibrosis transmembrane
 RT conductance regulator gene.";
 RL Genomics 10:301-307(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=91365359; PubMed=1716243;
 RA Yoritani T., Lemna W.K., Ballard C.F., Rosenbloom C.L., Rozmahel R.,
 RA Plevacic N., Tsui L.-C., Beaudet A.L.;
 RT "Molecular cloning and sequence analysis of the murine CFTR for the
 RT cystic fibrosis transmembrane conductance regulator.";
 RL Genomics 10:547-550(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=26122590; PubMed=10655503;
 RA Ellsworth R.E., Jamison D.C., Touchman J.W., Chisoe S.L.,
 RA Braden Maduro V.V., Bouffard G.G., Dietrich N.L.,
 RA Beckstrom-Sternberg S.M., Iyer L.W., Weintraub L.A., Cotton M.,
 RA Courtney L., Edwards J., Maupin R., Ozersky P., Rohlfing T.,
 RA Woldmann P., Miner T., Kemp R., Kramer J., Koff I., Pepin K.,
 RA Antonacci-Fulton L., Fulton R.S., Minx P., Hillier L.W., Wilson R.K.,
 RA Waterston R., Miller W., Green E.D.;
 RT "Comparative genomic sequence analysis of the human and mouse cystic
 RT fibrosis transmembrane conductance regulator genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1172-1177(2000).
 RN [4]
 RP SEQUENCE OF 1-17 FROM N.A.
 RX MEDLINE=95072572; PubMed=7526924;
 RA Denamur E., Chehab F.F.;
 RT "Analysis of the mouse and rat CFTR promoter regions.";
 RL Hum. Mol. Genet. 3:1089-1094(1994).
 RN [5]
 RP SEQUENCE OF 549-600 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Testis;
 RX MEDLINE=94004974; PubMed=7691356;
 RA Delaney S.J., Rich D.P., Thomson S.A., Hargrave M.R.,
 RA Lovelock P.K., Welsh M.J., Wainwright B.J.;
 RT "Cystic fibrosis transmembrane conductance regulator splice variants
 RT are not conserved and fail to produce chloride channels.";
 RL Nat. Genet. 4:426-431(1993).
 CC -1- FUNCTION: INVOLVED IN THE TRANSPORT OF CHLORIDE IONS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 1 (SHOWN HERE), 2 AND 3; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS EXPRESSED IN A VARIETY OF
 CC EPITHELIAL TISSUES INCLUDING COLON, KIDNEY, LUNG, SMALL
 CC INTESTINE AND TESTIS. ISOFORMS 2 AND 3 ARE EXPRESSED ONLY IN
 CC TESTIS.
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY, MRP SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: M69298; AAA37417.1; -
 CC EMBL: M60493; AAA18903.1; -
 CC EMBL: AF162137; AAF30300.1; -
 CC EMBL: I04873; AAA73562.1; -
 CC EMBL: S65942; AAB28393.1; -
 CC EMBL: S65940; AAB28393.1; JOINED.

DR EMBL: S65941; AAB28393.1; JOINED.
 DR EMBL: S65942; AAB28391.1; -
 DR EMBL: S65941; AAB28392.1; -
 DR EMBL: S65940; AAB28392.1; JOINED.
 DR PIR: A39901; A39901.
 DR PIR: A40303; A40303.
 DR HSSP: P13569; INBD.
 DR MSD: MGI:88388; Cfr.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR001140; ABCtransport.
 DR InterPro: IPR005291; CAMP_cl_channel.
 DR Pfam: PF00064; ABC_tran; 2.
 DR Pfam: PF00664; ABC_membrane; 2.
 DR ProDom: PD000006; ABC_transport; 2.
 DR SMART: SM00382; AAA; 2.
 DR TIGRfams: TIGR00953; 3a01202; 1.
 DR TIGRfams: TIGR01271; CTR_protein; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; transmembrane; transport; glycoprotein; Repeat;
 KW Ionic channel; phosphorylation; Alternative splicing.
 FT TRANSMEM 81 103
 FT TRANSMEM 118 138
 FT TRANSMEM 195 215
 FT TRANSMEM 221 241
 FT TRANSMEM 308 328
 FT TRANSMEM 331 350
 FT NP_BIND 458 465
 FT TRANSMEM 855 875
 FT TRANSMEM 907 927
 FT TRANSMEM 986 1006
 FT TRANSMEM 1009 1029
 FT TRANSMEM 1098 1118
 FT TRANSMEM 1124 1144
 FT NP_BIND 1240 1247
 FT CARBOHYD 889 889
 FT CARBOHYD 895 895
 FT VASPLIC 561 576
 FT VASPLIC 577 1476
 FT VASPLIC 561 600
 FT VASPLIC 601 1476
 FT CONFLICT 20 22
 FT CONFLICT 30 30
 FT CONFLICT 410 412
 FT CONFLICT 462 462
 FT CONFLICT 623 623
 FT CONFLICT 639 639
 SQ SEQUENCE 1476 AA; 167869 MW; 3D1B0BDD8DC1DA8 CRC64;
 Query Match 75.0%; Score 87; DB 1; Length 1476;
 Best Local Similarity 80.0%; Pred. No. 0.00053;
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 LEISEINEEDIKCECFDDM 21
 DB 813 INTEINEEDIKCECFDDV 832
 RESULT 8
 CSTR_SQUAC STANDARD: PRT: 1492 AA.
 ID CSTR_SQUAC P26362;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cystic fibrosis transmembrane conductance regulator (CFTR) (CAMP-
 DE dependent chloride channel).
 GN CSTR OR ABCCT.
 OS Squalus acanthias (Spiny dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

CC Elasmobranchii; Squalae; Squaloidae; Squalidae; Squalus.
 OX NCBI_TaxID=7797;
 (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92042226; PubMed=1718999;
 RA Marshall J., Martin K.A., Picciotto M., Hockfield S., Nairn A.C.,
 Kaczmarek L.K.;
 RT "Identification and localization of a dogfish homolog of human cystic
 fibrosis transmembrane conductance regulator.";
 RL J. Biol. Chem. 266:22749-22754(1991).
 CC -1- FUNCTION: INVOLVED IN THE TRANSPORT OF CHLORIDE IONS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
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 CC -----
 DR EMBL: M83785; AAA9616.1; -
 DR PIR: A39322; A39322.
 DR HSSP: P13569; 1MBD.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR003439; ABC_transporter.
 DR InterPro: IPR001140; ABCtransporter.
 DR InterPro: IPR005291; CAMP_channel.
 DR Pfam: PF00005; ABC_tran; 2.
 DR Pfam: PF00664; ABC_membrane; 2.
 DR ProDom: PD000006; ABC_transporter; 1.
 DR SMART: SM00382; AAA; 2.
 DR TIGRfam: TIGR00953; 3a01202; 1.
 DR TIGRfam: TIGR01271; Cfrp_protein; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; Transmembrane; Transport; Glycoprotein; Repeat;
 KW Ionic channel; Phosphorylation;
 FT TRANSMEM 82 104 1 (POTENTIAL).
 FT TRANSMEM 119 139 2 (POTENTIAL).
 FT TRANSMEM 156 216 3 (POTENTIAL).
 FT TRANSMEM 222 242 4 (POTENTIAL).
 FT TRANSMEM 309 329 5 (POTENTIAL).
 FT TRANSMEM 332 351 6 (POTENTIAL).
 FT NP_BIND 459 466 ATP (BY SIMILARITY).
 FT TRANSMEM 869 889 7 (POTENTIAL).
 FT TRANSMEM 926 946 8 (POTENTIAL).
 FT TRANSMEM 1005 1025 9 (POTENTIAL).
 FT TRANSMEM 1028 1048 10 (POTENTIAL).
 FT TRANSMEM 1117 1137 11 (POTENTIAL).
 FT TRANSMEM 1143 1163 12 (POTENTIAL).
 FT NP_BIND 1254 1261 ATP (BY SIMILARITY).
 FT CARBOHYD 905 905 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 923 923 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1492 AA; 169384 MW; 0E49CAB8968FC2F9 CRC64;
 Query Match 75.0%; Score 87; DB 1; Length 1492;
 Best Local Similarity 85.0%; Pred. No. 0.00054;
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 3 EISEEINEDDKCEFPDME 22
 DB 828 EISEEINEDDKCEFPDME 847
 RESULT 9
 LUXE_VIBHA
 ID LUXE_VIBHA STANDARD; PRT; 378 AA.
 AC P14286;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl)-

DE Protein synthetase).
 GN LUXE.
 OS Vibrrio harveyi.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrrio.
 OX NCBI_TaxID=669;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89374304; PubMed=2775296;
 RA Johnston T.C., Hruska K.S., Faughn Adams L.;
 RT "The nucleotide sequence of the luxE gene of Vibrrio harveyi and a
 RT comparison of the amino acid sequences of the acyl-protein
 RT synthetases from V. harveyi and V. fischeri.";
 RL Biochem. Biophys. Res. Commun. 163:93-101(1989).
 RN (2)
 CC SEQUENCE OF 370-378 FROM N.A.
 RX MEDLINE=90154014; PubMed=2303459;
 RA Swartzman E., Miyamoto C., Graham A., Meighen E.;
 RT "Delineation of the transcriptional boundaries of the lux operon of
 RT Vibrrio harveyi demonstrates the presence of two new lux genes.";
 RL J. Biol. Chem. 265:3513-3517(1990).
 CC -1- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
 CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
 CC FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
 CC SUBSTRATE IN THE LIPIDASE-CATALYZED REACTION.
 CC -1- CATALYTIC ACTIVITY: ATP + an acid + protein -> AMP + diphosphate +
 CC an acyl protein thioester.
 CC -1- PATHWAY: Biotransformation; fatty acid reduction system; second step.
 CC -1- SIMILARITY: WITH THE V. FISCHERI ACYL-PROTEIN SYNTHETASE.
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 CC -----
 DR EMBL: M28815; AAA27531.1; -
 DR DR M27139; -; NOT_ANNOTATED_CDS.
 DR PIR: A32916; A32916.
 DR PIR: A35081; A35081.
 KW Luminescence; Ligase.
 SQ SEQUENCE 378 AA; 42960 MW; 985DEA6E5425DB92 CRC64;
 Query Match 49.1%; Score 57; DB 1; Length 378;
 Best Local Similarity 45.0%; Pred. No. 1.4;
 Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 OY 3 EISEEINEDDKCEFPDME 22
 DB 265 QIRDFTNQELNLCFPEDE 284
 RESULT 10
 RN17_MOUSE
 ID RN17_MOUSE STANDARD; PRT; 626 AA.
 AC O99MW7;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE RING finger protein 17.
 GN RNF17.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=21175748; PubMed=11279525;
 RA Wang P.-J., McCarrey J.R., Yang F., Page D.C.;
 RT "An abundance of X-linked genes expressed in spermatogonia.";
 RL Nat. Genet. 27:422-426(2001).

CC -1- TISSUE SPECIFICITY: Testis-specific. Expressed only in male germ cells.

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

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CC -----

DR EMBL: AF285585; AAK31964.1; .

DR MGD: MGI:1353419; Rnf17.

DR InterPro: IPR001841; Znf_ring.

DR PROSITE: PS00518; ZF_RING_1; 1.

DR PROSITE: PS50089; ZF_RING_2; 1.

DR Zinc-finger.

FT ZN_FING 30 73 RING-TYPE.

SO SEQUENCE 626 AA; 69626 MW; 04B2BEC17AD734F CRC64;

Query Match 46.68; Score 54; DB 1; Length 626;

Best Local Similarity 64.78; Pred. No. 5.9; 4; Indels 0; Gaps 0;

Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 4 ISEINEDLEKCFDD 20

DB 398 IIEIIEENESCFTD 414

RESULT 11

ETFD_YEAST STANDARD; PRT; 631 AA.

AC 008822;

DT 01-NOV-1997 (Rel. 35, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE Probable electron transfer flavoprotein-ubiquinone oxidoreductase.

DE mitochondrial precursor (BC 1.5.5.1) (ETF-QO) (ETF-ubiquinone-oxidoreductase) (ETF dehydrogenase) (Electron-transfering-flavoprotein dehydrogenase).

GN YOR356W.

OS Saccharomyces cerevisiae (Baker's Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RA Delius H., Hebling U., Hofmann B.;

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: ACCEPTS ELECTRONS FROM ETF AND REDUCES UBIQUINONE (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: Reduced ETF + ubiquinone = ETF + ubiquinol.

CC -1- COFACTOR: FAD AND A 4FE-4S CLUSTER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By similarity).

CC -1- SIMILARITY: BELONGS TO THE ETF-QO / FIXC FAMILY.

CC -----

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CC -----

DR EMBL: Z75264; CAA9685.1; .

DR SGD: S0005883; YOR356W.

KW Oxidoreductase; Electron transport; Flavoprotein; FAD; Iron-sulfur; 4Fe-4S; Mitochondrion; Transit peptide; Ubiquinone.

FT TRANSIT 1 ?

FT CHAIN ? 631

PROBABLE ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE.

FT NP_BIND 65 79 FAD (ADP PART) (POTENTIAL).

FT METAL 574 574 IRON-SULFUR (4FE-4S) (POTENTIAL).

FT METAL 603 600 IRON-SULFUR (4FE-4S) (POTENTIAL).

FT METAL 603 603 IRON-SULFUR (4FE-4S) (POTENTIAL).

FT METAL 606 606 IRON-SULFUR (4FE-4S) (POTENTIAL).

SO SEQUENCE 631 AA; 69634 MW; 7493F67093D88391 CRC64;

Query Match 43.18; Score 50; DB 1; Length 631;

Best Local Similarity 47.48; Pred. No. 20;

Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 1 GLEISEINEDLEKCFD 19

DB 417 GLPVEEVEDDAMKMF 435

RESULT 12

ETXA_STAAM STANDARD; PRT; 257 AA.

AC P13163;

DT 01-JAN-1990 (Rel. 13, Created)

DT 15-JUN-1990 (Rel. 13, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Enterotoxin type A precursor (SEA).

GN ENTA OR MW1889.

OS Staphylococcus aureus (strain MW2), and

OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=196620, 1280;

ON [1]

RP SEQUENCE FROM N.A.

RC STRAIN-MW2;

RX MEDLINE=22040717; PubMed=12044378;

RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Nalini T., Kuroda H., Cui L., Yamamoto K., Hiratsuka K.,

RT "Genome and virulence determinants of high virulence community-acquired MRSA.";

RL Lancet 359:1819-1827(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-FR1337;

RX MEDLINE=88086892; PubMed=3335483;

RA Betty M.J., Mekalanos J.J.;

RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene.";

RL J. Bacteriol. 170:34-41(1988).

RN [3]

RP SEQUENCE OF 25-257.

RX MEDLINE=87222293; PubMed=3584106;

RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;

RT "Complete amino acid sequence of staphylococcal enterotoxin A.";

RL J. Biol. Chem. 262:7006-7015(1987).

RN [4]

RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

RX MEDLINE=95354648; PubMed=7628431;

RA Schae E.M., Zaitseva I., Zaitsev V.N., Dohlsten M., Kalland T., Schlievert P.M., Ohlendorf D.H., Svensson L.A.;

RT "Crystal structure of the superantigen staphylococcal enterotoxin type A.";

RL EMBO J. 14:3292-3301(1995).

RN [5]

RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).

RX MEDLINE=97113025; PubMed=8943278;

RA Sundstrom M., Hallen D., Svensson A., Schae E., Dohlsten M., Abrahamson L.;

RT "The Co-crystal structure of staphylococcal enterotoxin type A with Zn2+ at 2.7-A resolution. Implications for major histocompatibility complex class II binding.";

RL J. Biol. Chem. 271:32212-32216(1996).

RN [6]

RP 3D-STRUCTURE MODELING.

RX MEDLINE=96022987; PubMed=7552730;

RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;


```

RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins."
RL Net. Struct. Biol. 2:680-686(1995).
RN [7]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE-97334373; PubMed-9191070;
RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT "A structural and functional comparison of staphylococcal
RT enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity."
RL J. Mol. Biol. 269:270-280(1997).
CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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CC -----
CC EMBL: AF04828; BAB95754.1; -
CC PIR: A28664; A28664.1; -
CC PIR: A29566; A29566.
CC PDB: 1SEF; 1JUL-96.
CC PDB: 1SEA; 15-OCT-95.
CC PDB: 1SXT; 19-NOV-97.
CC InterPro: IPR001961; Strep/Strep_toxin.
CC DR Pfam: PF01123; Strep_Strep_toxin_1.
CC DR PRINTS: PR002876; Strep_toxin_C; 1.
CC DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
CC DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
CC DR Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
CC 3D-structure.
CC FT SIGNAL 1 24
CC FT CHAIN 25 257 ENTEROTOXIN TYPE A.
CC FT DISULFID 120 130
CC FT METAL 211 211 ZINC.
CC FT METAL 249 249 ZINC.
CC FT METAL 251 251 ZINC.
CC FT COMPLECT 242 242 T -> S (IN REF. 3).
CC SQ SEQUENCE 257 AA; 29669 MW; ADEBF5BCAIFL4677 CRC64;

Query Match 42.2%; Score 49; DB 1; Length 257;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GLEISEINEEDLKE 15
Db 24 GSEKSEINEKDLRK 38

RESULT 13
ETXE_STAAU STANDARD; PRT; 257 AA.
AC P12993;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JUN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Enterotoxin type E precursor (SEE).
GN ENTE.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

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OX NCBI_TaxID-1280;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
RC STRAIN-MJB265;
RX MEDLINE-88257005; PubMed-3384800;
RA Couch J.L., Solits M.T., Bellay M.J.;
RT "Cloning and nucleotide sequence of the type E staphylococcal
RT enterotoxin gene."
RL J. Bacteriol. 170:2954-2960(1988).
RN [2]
RP 3D-STRUCTURE MODELING.
RX MEDLINE-96022987; PubMed-7552730;
RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins."
RL Net. Struct. Biol. 2:680-686(1995).
CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II (By similarity).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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CC -----
CC EMBL: M21319; AAA26617.1; -
CC PIR: A28179; A28179.
CC PDB: 1SEE; 15-OCT-95.
CC InterPro: IPR001961; Strep/Strep_toxin.
CC DR Pfam: PF01123; Strep_Strep_toxin_1.
CC DR Pfam: PF02876; Strep_Strep_toxin_C; 1.
CC DR PRINTS: PR00279; BACTRTOXIN.
CC DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
CC DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
CC DR Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
CC 3D-structure.
CC FT SIGNAL 1 27
CC FT CHAIN 28 257 ENTEROTOXIN TYPE E.
CC FT METAL 211 211 ZINC (BY SIMILARITY).
CC FT METAL 249 249 ZINC (BY SIMILARITY).
CC FT METAL 251 251 ZINC (BY SIMILARITY).
CC SQ SEQUENCE 257 AA; 29358 MW; 27EDA94B97770CE3 CRC64;

Query Match 42.2%; Score 49; DB 1; Length 257;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GLEISEINEEDLKE 15
Db 24 GSEKSEINEKDLRK 38

RESULT 14
HEMN_HELPY STANDARD; PRT; 457 AA.
AC O25376;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Oxygen-independent coproporphyrinogen III oxidase (EC 1.-.-.-)
DE (Coproprophyrinogenase) (Coprophen oxidase).
GN HEHM OR HP0665.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID-210;

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RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-26695 / ATCC 700392;
RX  MEDLINE=97394467; PubMed=9252185;
RA  Tom J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA  Fleischman R.D., Ketchum K.A., Klein H.-P., Gill S., Dougherty B.A.,
RA  Nelson K., Quackenbush J., Zhou L., Kirnes E.F., Peterson S.,
RA  Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA  McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA  Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA  Cotton M.D., Meltman J.M., Fujii C., Bowman C., Matthey L., Wallin E.,
RA  Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA  Venter J.C.;
RT  "The complete genome sequence of the gastric pathogen Helicobacter
RT  pylori."
RL  Nature 388:539-547(1997);
CC  -1- FUNCTION: ANAEROBIC TRANSFORMATION OF COPROPORPHYRINOGEN-III INTO
CC  PROTOPORPHYRINOGEN-IX (BY SIMILARITY).
CC  -1- COFACITOR: REQUIRES MAGNESIUM, ATP AND NAD (OR NADP) FOR ACTIVITY.
CC  -1- PATHWAY: Porphyrin biosynthesis.
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC  -1- SIMILARITY: BELONGS TO THE ANAEROBIC COPROPORPHYRINOGEN III
CC  OXIDASE FAMILY.
CC  -----
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CC  -----
DR  EMBL: AE000579; AD07727.1; -
DR  TIGR: HP0665; -
DR  InterPro: IPR003401; Coprogen_an_ox.
DR  InterPro: IPR004558; HemN.
DR  Pfam: PF02473; Coprogen_an_ox; 1.
DR  TIGRfam: TIGR00538; hemN.1.
KW  Porphyrin biosynthesis; Oxidoreductase; Magnesium; NAD;
KW  Complete proteome.
SQ  SEQUENCE 457 AA; 53246 MW; 2578727AEFDE1218 CRC64;

Query Match 42.2%; Score 49; DB 1; Length 457;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 LEISEI-----NEEDLKECFDME 19
DB 26 VERNENFESLKTAFEN 43

RESULT 15
YHXB_BACSU STANDARD; PRT; 565 AA.
AC P18159;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update).
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable phosphomannomutase (EC 5.4.2.8) (PMW).
GN YHXB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RX MEDLINE=91178513; PubMed=2127799;
RA Holmberg C., Beijer L., Rutberg B., Rutberg L.;
RT "Glycerol catabolism in Bacillus subtilis: nucleotide sequence of the

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RP genes encoding glycerol kinase (glpK) and glycerol-3-phosphate
RT dehydrogenase (glpD)";
RL J. Gen. Microbiol. 136:2367-2375(1990).
CC -1- CATALYTIC ACTIVITY: D-mannose 1-phosphate -> D-mannose 6-phosphate.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOHEXOSE MUTASES FAMILY.
CC -----
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CC -----
DR EMBL: Y14079; CAAT4431.1; -
DR EMBL: M34393; AAA22488.1; -
DR EMBL: Z99108; CAB12759.1; -
DR EMBL: Z99109; CAB12770.1; -
DR PIR: S18566; S18566.
DR PIR: D45868; D45868.
DR Subtilist: BG10189; YHXB.
DR InterPro: IPR001485; PG/PMW_mutase.
DR Pfam: PF00408; PGW_PMW_1.
DR Pfam: PF02878; PGW_PMW_1.
DR Pfam: PF02879; PGW_PMW_11; 1.
DR Pfam: PF02880; PGW_PMW_111; 1.
DR PROSITE: PS00710; PGW_PMW_1.
KW Hypothetical protein; Isomerase; Phosphorylation; Complete proteome.
FT ACT_SITE 146 146
FT FORMS THE PHOSPHOSERINE INTERMEDIATE
FT (BY SIMILARITY).
SQ SEQUENCE 565 AA; 62901 MW; 34641A41232E1F07 CRC64;

Query Match 41.8%; Score 48.5; DB 1; Length 565;
Best Local Similarity 34.6%; Pred. No. 29;
Matches 9; Conservative 8; Mismatches 4; Indels 5; Gaps 1;

QY 2 LEISEI-----NEEDLKECFDME 22
DB 18 LELKRLLELGGDEALDECFYKIDE 43

Search completed: July 16, 2003, 14:01:41
Job time : 23 secs

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